

OIKE

# 2

## RAW SEQUENCE LISTING

DATE: 07/20/2001

PATENT APPLICATION: US/09/900,590

TIME: 11:25:41

Input Set : N:\Crif3\RULE60\09900590.txt

Output Set: N:\CRF3\07202001\I900590.raw

## SEQUENCE LISTING

**ENTERED**

Use

4 (1) GENERAL INFORMATION:

6 (i) APPLICANT: Huse, William D.

7 Glaser, Scott M.

9 (ii) TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human

10 Antibodies, Nucleic Acids Encoding Same and Methods of

12 (iii) NUMBER OF SEQUENCES: 100

14 (iv) CORRESPONDENCE ADDRESS:

15 (A) ADDRESSEE: Campbell & Flores LLP

16 (B) STREET: 4370 La Jolla Village Drive, Suite 700

17 (C) CITY: San Diego

18 (D) STATE: California

19 (E) COUNTRY: United States

20 (F) ZIP: 92122

22 (v) COMPUTER READABLE FORM:

23 (A) MEDIUM TYPE: Floppy disk

24 (B) COMPUTER: IBM PC compatible

25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

26 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

28 (vi) CURRENT APPLICATION DATA:

C--> 29 (A) APPLICATION NUMBER: US/09/900,590

C--> 30 (B) FILING DATE: 06-Jul-2001

31 (C) CLASSIFICATION:

33 (vii) PRIOR APPLICATION DATA:

34 (A) APPLICATION NUMBER: 09/016,061

35 (B) FILING DATE:

37 (viii) ATTORNEY/AGENT INFORMATION:

38 (A) NAME: Campbell, Cathryn A.

39 (B) REGISTRATION NUMBER: 31,815

40 (C) REFERENCE/DOCKET NUMBER: P-IX 2965

42 (ix) TELECOMMUNICATION INFORMATION:

43 (A) TELEPHONE: (619) 535-9001

44 (B) TELEFAX: (619) 535-8949

47 (2) INFORMATION FOR SEQ ID NO: 1:

49 (i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 351 base pairs

51 (B) TYPE: nucleic acid

52 (C) STRANDEDNESS: both

53 (D) TOPOLOGY: linear

56 (ix) FEATURE:

57 (A) NAME/KEY: CDS

58 (B) LOCATION: 1..351

61 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

63 CAG GTG CAG CTG GTG GAG TCT GGG GGA GGC GTT GTG CAG CCT GGA AGG 48

64 Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

65 1 5 10 15

67 TCC CTG AGA CTC TCC TGT GCA GCC TCT GGA TTC ACC TTC AGT AGC TAT 96

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68 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
69          20          25          30
71 GAC ATG TCT TGG GTT CGC CAG GCT CCG GGC AAG GGT CTG GAG TGG GTC      144
72 Asp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
73          35          40          45
75 GCA AAA GTT AGT AGT GGT GGT GGT AGC ACC TAC TAT TTA GAC ACT GTG      192
76 Ala Lys Val Ser Ser Gly Gly Gly Ser Thr Tyr Tyr Leu Asp Thr Val
77          50          55          60
79 CAG GGC CGA TTC ACC ATC TCC AGA GAC AAT AGT AAG AAC ACC CTA TAC      240
80 Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
81 65          70          75          80
83 CTG CAA ATG AAC TCT CTG AGA GCC GAG GAC ACA GCC GTG TAT TAC TGT      288
84 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85          85          90          95
87 GCA AGA CAT AAC TAC GGC AGT TTT GCT TAC TGG GGC CAA GGG ACT ACA      336
88 Ala Arg His Asn Tyr Gly Ser Phe Ala Tyr Trp Gly Gln Gly Thr Thr
89          100          105          110
91 GTG ACT GTT TCT AGT      351
92 Val Thr Val Ser Ser
93          115
96 (2) INFORMATION FOR SEQ ID NO: 2:
98   (i) SEQUENCE CHARACTERISTICS:
99       (A) LENGTH: 117 amino acids
100       (B) TYPE: amino acid
101       (D) TOPOLOGY: linear
103   (ii) MOLECULE TYPE: protein
105   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
107 Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
108 1          5          10          15
110 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
111          20          25          30
113 Asp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
114          35          40          45
116 Ala Lys Val Ser Ser Gly Gly Gly Ser Thr Tyr Tyr Leu Asp Thr Val
117          50          55          60
119 Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
120 65          70          75          80
122 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
123          85          90          95
125 Ala Arg His Asn Tyr Gly Ser Phe Ala Tyr Trp Gly Gln Gly Thr Thr
126          100          105          110
128 Val Thr Val Ser Ser
129          115
131 (2) INFORMATION FOR SEQ ID NO: 3:
133   (i) SEQUENCE CHARACTERISTICS:
134       (A) LENGTH: 321 base pairs
135       (B) TYPE: nucleic acid
136       (C) STRANDEDNESS: both
137       (D) TOPOLOGY: linear

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140      (ix) FEATURE:
141          (A) NAME/KEY: CDS
142          (B) LOCATION: 1..321
143      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
144      GAG ATT GTG CTA ACT CAG TCT CCA GCC ACC CTG TCT CTC AGC CCA GGA      48
145      Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
146      1      5      10      15
147      GAA AGG GCG ACT CTT TCC TGC CAG GCC AGC CAA AGT ATT AGC AAC CAC      96
148      Glu Arg Ala Thr Leu Ser Cys Gln Ala Ser Gln Ser Ile Ser Asn His
149      20      25      30
150      CTA CAC TGG TAT CAA CAA AGG CCT GGT CAA GCC CCA AGG CTT CTC ATC      144
151      Leu His Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Leu Ile
152      35      40      45
153      AAG TAT CGT TCC CAG TCC ATC TCT GGG ATC CCC GCC AGG TTC AGT GGC      192
154      Lys Tyr Arg Ser Gln Ser Ile Ser Gly Ile Pro Ala Arg Phe Ser Gly
155      50      55      60
156      AGT GGA TCA GGG ACA GAT TTC ACC CTC ACT ATC TCC AGT CTG GAG CCT      240
157      Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
158      65      70      75      80
159      GAA GAT TTT GCA GTC TAT TAC TGT CAA CAG AGT GGC AGC TGG CCT CAC      288
160      Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Ser Gly Ser Trp Pro His
161      85      90      95
162      ACG TTC GGA GGG GGG ACC AAG GTG GAA ATT AAG      321
163      Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
164      100      105
165      (2) INFORMATION FOR SEQ ID NO: 4:
166      (i) SEQUENCE CHARACTERISTICS:
167          (A) LENGTH: 107 amino acids
168          (B) TYPE: amino acid
169          (D) TOPOLOGY: linear
170      (ii) MOLECULE TYPE: protein
171      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
172      Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
173      1      5      10      15
174      Glu Arg Ala Thr Leu Ser Cys Gln Ala Ser Gln Ser Ile Ser Asn His
175      20      25      30
176      Leu His Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Leu Ile
177      35      40      45
178      Lys Tyr Arg Ser Gln Ser Ile Ser Gly Ile Pro Ala Arg Phe Ser Gly
179      50      55      60
180      Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
181      65      70      75      80
182      Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Ser Gly Ser Trp Pro His
183      85      90      95
184      Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
185      100      105
186      (2) INFORMATION FOR SEQ ID NO: 5:
187      (i) SEQUENCE CHARACTERISTICS:
188          (A) LENGTH: 351 base pairs

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212      (B) TYPE: nucleic acid
213      (C) STRANDEDNESS: both
214      (D) TOPOLOGY: linear
217      (ix) FEATURE:
218          (A) NAME/KEY: CDS
219          (B) LOCATION: 1..351
222      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
224 GAA GTG CAG CTG GTG GAG TCT GGG GGA GGC TTA GTG AAG CCT GGA AGG      48
225 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Arg
226   1          5          10          15
228 TCC CTG AGA CTC TCC TGT GCA GCC TCT GGA TTC GCT TTC AGT AGC TAT      96
229 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ala Phe Ser Ser Tyr
230          20          25          30
232 GAC ATG TCT TGG GTT CGC CAG ATT CCG GAG AAG AGG CTG GAG TGG GTC      144
233 Asp Met Ser Trp Val Arg Gln Ile Pro Glu Lys Arg Leu Glu Trp Val
234          35          40          45
236 GCA AAA GTT AGT AGT GGT GGT GGT AGC ACC TAC TAT TTA GAC ACT GTG      192
237 Ala Lys Val Ser Ser Gly Gly Gly Ser Thr Tyr Tyr Leu Asp Thr Val
238          50          55          60
240 CAG GGC CGA TTC ACC ATC TCC AGA GAC AAT GCC AAG AAC ACC CTA TAC      240
241 Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
242   65          70          75          80
244 CTG CAA ATG AGC AGT CTG AAC TCT GAG GAC ACA GCC ATG TAT TAC TGT      288
245 Leu Gln Met Ser Ser Leu Asn Ser Glu Asp Thr Ala Met Tyr Tyr Cys
246          85          90          95
248 GCA AGA CAT AAC TAC GGC AGT TTT GCT TAC TGG GGC CAA GGG ACT CTG      336
249 Ala Arg His Asn Tyr Gly Ser Phe Ala Tyr Trp Gly Gln Gly Thr Leu
250          100          105          110
252 GTC ACT GTC TCT GCA      351
253 Val Thr Val Ser Ala
254          115
257 (2) INFORMATION FOR SEQ ID NO: 6:
259      (i) SEQUENCE CHARACTERISTICS:
260          (A) LENGTH: 117 amino acids
261          (B) TYPE: amino acid
262          (D) TOPOLOGY: linear
264      (ii) MOLECULE TYPE: protein
266      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
268 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Arg
269   1          5          10          15
271 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ala Phe Ser Ser Tyr
272          20          25          30
274 Asp Met Ser Trp Val Arg Gln Ile Pro Glu Lys Arg Leu Glu Trp Val
275          35          40          45
277 Ala Lys Val Ser Ser Gly Gly Gly Ser Thr Tyr Tyr Leu Asp Thr Val
278          50          55          60
280 Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
281   65          70          75          80
283 Leu Gln Met Ser Ser Leu Asn Ser Glu Asp Thr Ala Met Tyr Tyr Cys

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Input Set : N:\Crf3\RULE60\09900590.txt

Output Set: N:\CRF3\07202001\I900590.raw

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284                      85                      90                      95
286 Ala Arg His Asn Tyr Gly Ser Phe Ala Tyr Trp Gly Gln Gly Thr Leu
287                      100                      105                      110
289 Val Thr Val Ser Ala
290                      115
292 (2) INFORMATION FOR SEQ ID NO: 7:
294   (i) SEQUENCE CHARACTERISTICS:
295       (A) LENGTH: 321 base pairs
296       (B) TYPE: nucleic acid
297       (C) STRANDEDNESS: both
298       (D) TOPOLOGY: linear
301   (ix) FEATURE:
302       (A) NAME/KEY: CDS
303       (B) LOCATION: 1..321
306   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
308 GAT ATT GTG CTA ACT CAG TCT CCA GCC ACC CTG TCT GTG ACA CCA GGA      48
309 Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Val Thr Pro Gly
310 1      5      10      15
312 GAT AGC GTC AGT CTT TCC TGC CAG GCC AGC CAA AGT ATT AGC AAC CAC      96
313 Asp Ser Val Ser Leu Ser Cys Gln Ala Ser Gln Ser Ile Ser Asn His
314      20      25      30
316 CTA CAC TGG TAT CAA CAA AAA TCA CAT GAG TCT CCA AGG CTT CTC ATC      144
317 Leu His Trp Tyr Gln Gln Lys Ser His Glu Ser Pro Arg Leu Leu Ile
318      35      40      45
320 AAG TAT CGT TCC CAG TCC ATC TCT GGG ATC CCC TCC AGG TTC AGT GGC      192
321 Lys Tyr Arg Ser Gln Ser Ile Ser Gly Ile Pro Ser Arg Phe Ser Gly
322      50      55      60
324 AGT GGA TCA GGG ACA GAT TTC GCT CTC AGT ATC AAC AGT GTG GAG ACT      240
325 Ser Gly Ser Gly Thr Asp Phe Ala Leu Ser Ile Asn Ser Val Glu Thr
326 65      70      75      80
328 GAA GAT TTT GGA ATG TAT TTC TGT CAA CAG AGT GGC AGC TGG CCT CAC      288
329 Glu Asp Phe Gly Met Tyr Phe Cys Gln Gln Ser Gly Ser Trp Pro His
330      85      90      95
332 ACG TTC GGA GGG GGG ACC AAG CTG GAA ATT AAG      321
333 Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys
334      100      105
337 (2) INFORMATION FOR SEQ ID NO: 8:
339   (i) SEQUENCE CHARACTERISTICS:
340       (A) LENGTH: 107 amino acids
341       (B) TYPE: amino acid
342       (D) TOPOLOGY: linear
344   (ii) MOLECULE TYPE: protein
346   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
348 Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Val Thr Pro Gly
349 1      5      10      15
351 Asp Ser Val Ser Leu Ser Cys Gln Ala Ser Gln Ser Ile Ser Asn His
352      20      25      30
354 Leu His Trp Tyr Gln Gln Lys Ser His Glu Ser Pro Arg Leu Leu Ile
355      35      40      45

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/900,590

DATE: 07/20/2001

TIME: 11:25:42

Input Set : N:\Crf3\RULE60\09900590.txt

Output Set: N:\CRF3\07202001\I900590.raw

L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]

L:738 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31

L:774 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32